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Processing characteristics of dairy cow milk are moderately heritable

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ABSTRACT

Milk processing attributes represent a group of milk quality traits that are important to the dairy industry to inform product portfolio. However, because of the resources required to routinely measure such quality traits, precise genetic parameter estimates from a large population of animals are lacking for these traits. Milk processing characteristics considered in the present study—rennet coagulation time, curd-firming time, curd firmness at 30 and 60 min after rennet addition, heat coagulation time, casein micelle size, and milk pH—were all estimated using mid-infrared spectroscopy prediction equations. Variance components for these traits were estimated using 136,807 test-day records from 5 to 305 d in milk (DIM) from 9,824 cows using random regressions to model the additive genetic and within-lactation permanent environmental variances. Heritability estimates ranged from 0.18 ± 0.01 (26 DIM) to 0.38 ± 0.02 (180 DIM) for rennet coagulation time; from 0.26 ± 0.02 (5 DIM) to 0.57 ± 0.02 (174 DIM) for curd-firming time; from 0.16 ± 0.01 (30 DIM) to 0.56 ± 0.02 (271 DIM) for curd firmness at 30 min; from 0.13 ± 0.01 (30 DIM) to 0.48 ± 0.02 (271 DIM) for curd firmness at 60 min; from 0.08 ± 0.01 (17 DIM) to 0.24 ± 0.01 (180 DIM) for heat coagulation time; from 0.23 ± 0.02 (30 DIM) to 0.43 ± 0.02 (261 DIM) for casein micelle size; and from 0.20 ± 0.01 (30 DIM) to 0.36 ± 0.02 (151 DIM) for milk pH. Within-trait genetic correlations across DIM weakened as the number of days between compared intervals increased but were mostly >0.4 except between the peripheries of the lactation. Eigenvalues and associated eigenfunctions of the additive genetic covariance matrix for all traits revealed that at least the 80% of the genetic variation among animals in lactation profiles was associated with the height of the lactation profile. Curd-firming time and curd firmness at 30 min were weakly to moderately genetically correlated with milk yield (from 0.33 ± 0.05 to 0.59 ± 0.05 for curd-firming time, and from −0.62 ± 0.03 to −0.21 ± 0.06 for curd firmness at 30 min). Milk protein concentration was strongly genetically correlated with curd firmness at 30 min (0.84 ± 0.02 to 0.94 ± 0.01) but only weakly genetically correlated with milk heat coagulation time (−0.27 ± 0.07 to 0.19 ± 0.06). Results from the present study indicate the existence of exploitable genetic variation for milk processing characteristics. Because of possible indirect deterioration in milk processing characteristics due to selection for greater milk yield, emphasis on milk processing characteristics is advised.

Key words: milk coagulation, milk quality, milk technological, spectrometry, random regression

INTRODUCTION

The importance of milk composition and udder health in the production of dairy products is generally well accepted (Williams, 2003; Murphy et al., 2016). Such importance underpins the inclusion of both milk composition and udder health in several dairy cow breeding objectives globally (Miglior et al., 2005). However, milk processability, which dictates the potential of transforming milk into different dairy products such as cheese and milk powder, is also an important characteristic of milk composition. Despite this, milk processability is not explicitly considered in national dairy cow breeding objectives.

Indicators of milk processability are commonly referred to as milk coagulation properties and these include rennet coagulation time (**RCT**, min), curd-firming time ($\mathbf{k_{20}}$, min), curd firmness 30 ($\mathbf{a_{30}}$, mm) and 60 ($\mathbf{a_{60}}$, mm) min after rennet addition, and heat coagulation time (**HCT**, min), casein micelle size (**CMS**, nm), and milk pH. Several factors are known to contribute to variability in milk processing characteristics such as cow breed (De Marchi et al., 2007; Poulsen et al., 2013; Chen et al., 2016), stage of lactation (Ikonen et al., 2004; Barłowska et al., 2014), parity number (Ikonen et al., 1999; Tyrisevä et al., 2004), and the diet ingested

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(Reid et al., 2015). The existence of genetic variation in milk coagulation properties has been documented in several Holstein-Friesian populations, including populations in Italy (1,042 cows, Cassandro et al., 2008), Estonia (4,191 cows, Vallas et al., 2010; 5,216 cows, Pretto et al., 2014), Denmark (357 cows; Poulsen et al., 2015), and Finland (399 cows, Tyrisevä et al., 2004). These studies, however, have been limited in size, contributing to large associated standard errors of the estimated (co) variance components, and they have estimated genetic parameters of milk coagulation properties using repeatability animal models. The exceptions to the latter are Vallas et al. (2010) and Pretto et al. (2014), which used random regression animal models. To our knowledge, no study has attempted to quantify the existence of genetic variation in either HCT or CMS in dairy cows.

Large-scale recording of milk processing traits is often hampered by the associated resources necessary to undertake the reference methodologies. This not only limits the data set sizes to estimate precise genetic parameters, but also precludes the implementation of breeding strategies to improve these characteristics directly. Milk mid-infrared spectroscopy has been proposed as a phenotyping tool for a multitude of animal characteristics (Bastin et al., 2016; McParland and Berry, 2016) and milk quality traits (De Marchi et al., 2014), including milk processing attributes (Visentin et al., 2015). One of the main advantages of mid-infrared spectroscopy is that, once developed, new prediction models can be applied to historical spectral data for the prediction of novel traits at no additional cost.

Therefore, the objective of the present study was to quantify the genetic variation in milk processing characteristics and their correlations with milk-related performance traits using random regression models fitted across lactation. Results of the present study will provide greater and more precise knowledge of the extent of genetic variability that exists in milk processing characteristics and how this changes across lactation.

MATERIALS AND METHODS

Data

Milk samples used in the present study originated from 76 Irish herds collected between January 2013 and December 2015, inclusive; 174,062 milk samples from 10,394 dairy cows were collected.

Sixty-nine of the aforementioned 76 farms were commercial herds located in the Munster region of Ireland; the average herd size was 126 cows. Animals in the commercial herds were milked twice a day, at approximately 0700 h (a.m.) and again at approximately 1500 h (p.m.), and a combined a.m.+p.m. individual milk sample was sporadically collected and sent to the laboratory of Teagasc Animal and Grassland Research and Innovation Center (Moorepark, Fermoy, Co. Cork, Ireland) for mid-infrared spectroscopy analysis. On average, 1,249 samples were analyzed each month. Milk yield of the commercial farms represented the entire daily milk produced during the test-day recording. The average number of collected milk samples per cow was 5.15, and 14,873 lactation records were available.

The remaining 7 farms were operated by Teagasc Animal and Grassland Research and Innovation Center (Moorepark, Fermoy, Co. Cork). In these research herds, 1,661 dairy cows were participating in various experimental treatments based on different feeding strategies and management practices, including various stocking rates, calving periods, and lengths of grazing period. All cows were fed a basal diet of grazed pasture, but at times were offered a quantity of concentrates according to the experimental treatment. Animals were milked twice a day (a.m. and p.m.) and milk yield was recorded at each milking session. Milk yield of the 2 daily milking sessions was summed to obtain daily milk yield. Individual milk samples were taken separately, once weekly, on consecutive p.m. and a.m. milkings. The average number of milk samples collected per cow was 78, and the total number of lactations available was 2,956.

Spectra information and milk chemical composition (i.e., concentrations of protein, casein, fat, lactose, total solids, and urea) of all milk samples were generated using the same MilkoScan FT6000 (Foss Electric A/S, Hillerød, Denmark) in the laboratory of Teagasc Animal and Grassland Research and Innovation Center (Moorepark, Fermoy, Co. Cork, Ireland) within a week of sample collection. The resulting milk spectra, containing 1,060 transmittance data points in the region between 900 and 5,000 cm^{-1}, were stored. Somatic cell count of all samples was determined using a Fossomatic (Foss Electric A/S).

Prediction of Milk Processing Phenotype

Between the years 2013 and 2014, a calibration data set was generated from individual bovine milk samples collected from the 7 Irish research herds as described in detail by Visentin et al. (2015); data from cows milking in these 7 research farms also contributed to the larger data set in the present study. Full details on the development of the mid-infrared spectroscopy prediction models for milk technological traits, including RCT, k_{20}, a_{30}, a_{60}, HCT, CMS, and pH are reported by Visentin et al. (2015). Rennet coagulation time represents the time required to induce milk coagulation after rennet addition, k_{20} is the time between the gel development and